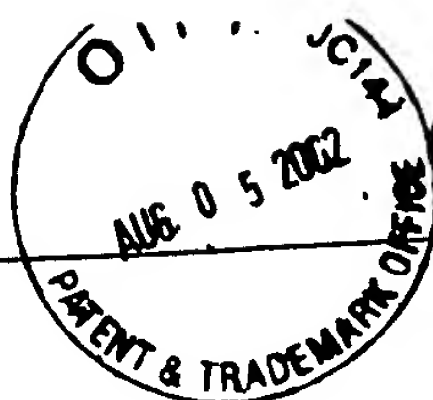


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2002-07-29 Sequence.txt  
SEQUENCE LISTING

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<110> M&E Biotech A/S

<120> Method for down-regulating GDF-8 activity

<130> 3631-0117P

<140> 09/620,586

<141> 2000-07-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 375

<212> PRT

<213> Homo sapiens

<400> 1

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20 25 30  
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
35 40 45  
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60  
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu  
65 70 75 80  
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95  
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110  
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu  
115 120 125  
Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser

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130																
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145					150					155					160	
Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195					200					205				
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	
225					230					235					240	
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
				245					250					255		
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	
305					310					315					320	
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	
				325					330					335		
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	
			340					345					350			
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	
		355					360					365				
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<210> 2

<211> 362

<212> PRT

<213> Meleagris gallopavo

<400> 2

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Thr	Glu	Asn	Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	20	25	30	
Gln	Asn	Thr	Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	35	40	45	
Ser	Lys	Leu	Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	50	55	60	
Lys	Gln	Leu	Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	65	70	75	80
Tyr	Asp	Val	Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	85	90	95	
Asp	Tyr	His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	100	105	110	
Asp	Phe	Leu	Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	115	120	125	
Phe	Ser	Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	130	135	140	
Ile	Tyr	Leu	Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	145	150	155	160
Leu	Arg	Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	165	170	175	
Arg	Ser	Leu	Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	180	185	190	
Ile	Asp	Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	195	200	205	
Asn	Leu	Gly	Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Asn	Gly	Arg	Asp	Leu	210	215	220	

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Ala Val Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu  
 225 230 235 240

Glu Val Arg Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly  
 245 250 255

Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro  
 260 265 270

Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro  
 275 280 285

Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe  
 290 295 300

Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg  
 305 310 315 320

Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn  
 325 330 335

Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro  
 340 345 350

Ala Met Val Val Asp Arg Cys Gly Cys Ser  
 355 360

<210> 3  
 <211> 375  
 <212> PRT  
 <213> Gallus sp.

<400> 3  
 Met Gln Lys Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile  
 1 5 10 15

Ala Val Asp Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn  
 20 25 30

Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
 35 40 45

Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
 50 55 60

Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu  
 65 70 75 80

## 2002-07-29 Sequence.txt

Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	85	90	95
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	100	105	110
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	115	120	125
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	130	135	140
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	145	150	155
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	165	170	175
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	180	185	190
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	195	200	205
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	210	215	220
Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Thr	Gly	Arg	Asp	Leu	Ala	Val	Thr	225	230	235
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	245	250	255
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	260	265	270
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	275	280	285
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	290	295	300
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	305	310	315
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	325	330	335

2002-07-29 Sequence.txt

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
 340 345 350

Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
 355 360 365

Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 4

<211> 376

<212> PRT

<213> Mus musculus

<400> 4

Met Met Gln Lys Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu  
 1 5 10 15

Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu  
 20 25 30

Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn  
 35 40 45

Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys  
 50 55 60

Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln  
 65 70 75 80

Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp  
 85 90 95

Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr  
 100 105 110

His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe  
 115 120 125

Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser  
 130 135 140

Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr  
 145 150 155 160

Leu Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg

165

170

175

Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser  
 180 185 190  
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp  
 195 200 205  
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu  
 210 215 220  
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val  
 225 230 235 240  
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val  
 245 250 255  
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp  
 260 265 270  
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
 275 280 285  
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
 290 295 300  
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln  
 305 310 315 320  
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser  
 325 330 335  
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
 340 345 350  
 Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met  
 355 360 365  
 Val Val Asp Arg Cys Gly Cys Ser  
 370 375

&lt;210&gt; 5

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Bos taurus

&lt;400&gt; 5

2002-07-29 Sequence.txt

Met Gln Lys Leu Gln Ile Ser Val Tyr Ile Tyr Leu Phe Met Leu Ile  
1 5 10 15

Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr  
35 40 45

Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val  
85 90 95

Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110

Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu  
115 120 125

Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
130 135 140

Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu  
145 150 155 160

Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu  
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
225 230 235 240

Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys  
245 250 255



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Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
260 265 270

Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
275 280 285

Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
290 295 300

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
305 310 315 320

Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
325 330 335

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
340 345 350

Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
355 360 365

Val Asp Arg Cys Gly Cys Ser  
370 375

<210> 6

<211> 375

<212> PRT

<213> Ovis sp.

<400> 6

Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu  
1 5 10 15

Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
20 25 30

Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn  
35 40 45

Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95

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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
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Val	Thr	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
			115					120					125			
Ala	Glu	Val	Gln	Glu	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
			130					135					140			
Lys	Ile	Gln	His	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
						150					155				160	
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
						165					170				175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
						180							190			
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
						195						205				
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
						215						220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	
						230					235				240	
Phe	Pro	Glu	Pro	Gly	Glu	Glu	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
						245					250				255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
						260							270			
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
						275						285				
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
						295						300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Leu	Phe	Leu	Gln	Lys	
						310					315				320	
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Lys	Gly	Ser	Ala	
						325					330				335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	
						340					345			350		

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Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val  
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Val Asp Arg Cys Gly Cys Ser  
 370 375

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 <211> 376  
 <212> PRT  
 <213> Rattus norvegicus

<400> 7  
 Met Ile Gln Lys Pro Gln Met Tyr Val Tyr Ile Tyr Leu Phe Val Leu  
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Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Asp Ser Glu Arg Glu Ala  
 20 25 30

Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn  
 35 40 45

Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys  
 50 55 60

Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln  
 65 70 75 80

Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp  
 85 90 95

Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr  
 100 105 110

His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe  
 115 120 125

Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser  
 130 135 140

Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr  
 145 150 155 160

Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg  
 165 170 175

Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser

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180

185

190

Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp  
195 200 205

Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu  
210 215 220

Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val  
225 230 235 240

Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val  
245 250 255

Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp  
260 265 270

Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
275 280 285

Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
290 295 300

Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln  
305 310 315 320

Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser  
325 330 335

Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
340 345 350

Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met  
355 360 365

Val Val Asp Arg Cys Gly Cys Ser  
370 375

<210> 8

<211> 375

<212> PRT

<213> Sus scrofa

<400> 8

Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile  
1 5 10 15

Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr  
35 40 45

Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110

Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu  
115 120 125

Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
130 135 140

Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
145 150 155 160

Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu  
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
225 230 235 240

Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys  
245 250 255

Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
260 265 270

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Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
 275 280 285

Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
 290 295 300

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
 305 310 315 320

Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
 340 345 350

Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
 355 360 365

Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 9  
 <211> 374  
 <212> PRT  
 <213> Danio rerio

<400> 9  
 Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys  
 1 5 10 15

Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr  
 20 25 30

Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His  
 35 40 45

Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys  
 50 55 60

Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln  
 65 70 75 80

Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp  
 85 90 95

Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu  
 100 105 110

2002-07-29 Sequence.txt

His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro  
115 120 125

Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser  
130 135 140

Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His  
145 150 155 160

Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg  
165 170 175

Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys  
180 185 190

Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys  
195 200 205

Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile  
210 215 220

Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser  
225 230 235 240

Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile  
245 250 255

Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp  
260 265 270

Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp  
275 280 285

Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys  
290 295 300

Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr  
305 310 315 320

Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly  
325 330 335

Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe  
340 345 350

Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val  
355 360 365

Asp Arg Cys Gly Cys Ser  
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<210> 10  
<211> 375  
<212> PRT  
<213> Papio hamadryas

<400> 10  
Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile  
1 5 10 15  
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
20 25 30  
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
35 40 45  
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60  
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
65 70 75 80  
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95  
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110  
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu  
115 120 125  
Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
130 135 140  
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
145 150 155 160  
Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu  
165 170 175  
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
180 185 190  
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val



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195

200

205

Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
210						215					220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
225					230					235					240
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys
				245					250					255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
			260					265					270		
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
		275					280					285			
Asp	Phe	Glu	Ala	Leu	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
	290					295					300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
305					310					315					320
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
				325					330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
			340					345					350		
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val
		355					360					365			
Val	Asp	Arg	Cys	Gly	Cys	Ser									
	370					375									

<210> 11

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(109)

<223> Identical to residues 267-375 in SEQ ID NO: 1

<400> 11

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys

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1              5              10              15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
      20              25              30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
      35              40              45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
      50              55              60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
      65              70              75              80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
      85              90              95
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
      100              105

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<210> 12
<211> 109
<212> PRT
<213> Bos taurus

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<220>
<221> PEPTIDE
<222> (1)..(109)
<223> Identical to residues 267-375 in SEQ ID NO: 5

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<400> 12
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
  1              5              10              15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
      20              25              30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
      35              40              45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
      50              55              60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
      65              70              75              80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly

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Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
 100 105

<210> 13  
 <211> 15  
 <212> PRT  
 <213> Clostridium tetani

<400> 13  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
 1 5 10 15

<210> 14  
 <211> 21  
 <212> PRT  
 <213> Clostridium tetani

<400> 14  
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
 1 5 10 15

Ala Ser His Leu Glu  
 20

<210> 15  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (18)..(32)  
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
 <221> SIMILAR  
 <222> (1)..(17)  
 <223> Identical to residues 267-283 in SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (33)..(109)  
 <223> Identical to residues 299-375 in SEQ ID NO: 1

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<220>  
 <221> SITE  
 <222> (73)  
 <223> Cys or Ser

<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly

<400> 15  
 Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
           1                          5                          10                          15

Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
                           20                          25                          30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
                           35                          40                          45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
                           50                          55                          60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
                           65                          70                          75                          80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
                           85                          90                          95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
                           100                          105

<210> 16  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (52)..(66)  
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
 <221> SIMILAR  
 <222> (1)..(51)  
 <223> Identical to residues 267-317 in SEQ ID NO: 1

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<220>  
 <221> SIMILAR  
 <222> (67)..(109)  
 <223> Identical to residues 333-375 in SEQ ID NO: 1

<220>  
 <221> SITE  
 <222> (73)  
 <223> Cys or Ser

<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly

<400> 16  
 Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
   1                  5                  10                  15  
 Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
                   20                  25                  30  
 Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
                   35                  40                  45  
 Phe Val Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr  
           50                  55                  60  
 Glu Leu Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
   65                  70                  75                  80  
 Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
                   85                  90                  95  
 Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
                   100                  105

<210> 17  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (83)..(97)  
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

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<220>

<221> SIMILAR

<222> (1)..(82)

<223> Identical to residues 267-348 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (98)..(109)

<223> Identical to residues 364-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 17

Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys
1				5					10					15	

Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile
			20					25					30		

Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu
		35					40					45			

Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala
	50					55					60				

Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser
65					70					75				80	

Pro	Ile	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu
				85					90					95	

Leu	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser
			100					105				

<210> 18

<211> 109

<212> PRT

<213> Artificial sequence

2002-07-29 Sequence.txt

<220>

<221> MUTAGEN

<222> (21)..(41)

<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>

<221> SIMILAR

<222> (42)..(109)

<223> Identical to residues 307-375 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (42)..(109)

<223> Identical to residues 308-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 18

Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys
1				5					10					15	

Arg	Tyr	Pro	Leu	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val
			20					25					30		

Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Tyr	Cys	Ser	Gly	Glu	Cys	Glu
		35					40					45			

Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala
	50					55					60				

Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser
65					70					75				80	

Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly
			85						90					95	

Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser
			100				105					

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<210> 19  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (49)..(69)  
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
 <221> SIMILAR  
 <222> (1)..(48)  
 <223> Identical to residues 267-314 in SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (70)..(109)  
 <223> Identical to residues 336-375 in SEQ ID NO: 1

<220>  
 <221> SITE  
 <222> (73)  
 <223> Cys or Ser

<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly

<400> 19  
 Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
   1                  5                  10                  15  
 Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
           20                  25                  30  
 Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
           35                  40                  45  
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
       50                  55                  60  
 Ala Ser His Leu Glu Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
   65                  70                  75                  80  
 Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
           85                  90                  95



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Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 20  
<211> 109  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (79)..(99)  
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
<221> SIMILAR  
<222> (1)..(78)  
<223> Identical to residues 267-345 in SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (100)..(109)  
<223> Identical to residues 366-375 in SEQ ID NO: 1

<220>  
<221> SITE  
<222> (73)  
<223> Cys or Ser

<220>  
<221> SITE  
<222> (90)..(91)  
<223> Lys Glu or Glu Gly

<400> 20  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Phe Asn

65

70

75

80

Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser  
                             85                            90                            95

His Leu Glu Ala Met Val Val Asp Arg Cys Gly Cys Ser  
                             100                            105

&lt;210&gt; 21

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;221&gt; MUTAGEN

&lt;222&gt; (84)..(104)

&lt;223&gt; Tetanus toxoid P30 epitope (SEQ ID NO: 14)

&lt;220&gt;

&lt;221&gt; SIMILAR

&lt;222&gt; (1)..(83)

&lt;223&gt; Identical to residues 267-349 in SEQ ID NO: 1

&lt;220&gt;

&lt;221&gt; SIMILAR

&lt;222&gt; (105)..(109)

&lt;223&gt; Identical to residues 371-375 in SEQ ID NO: 1

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (73)

&lt;223&gt; Cys or Ser

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (90)..(91)

&lt;223&gt; Lys Glu or Glu Gly

&lt;400&gt; 21

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
   1                            5                            10                            15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
                             20                            25                            30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
                             35                            40                            45

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Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro  
85 90 95

Lys Val Ser Ala Ser His Leu Glu Arg Cys Gly Cys Ser  
100 105

<210> 22  
<211> 254  
<212> PRT  
<213> Artificial sequence

<220>  
<221> SIMILAR  
<222> (110)..(124)  
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
<221> SIMILAR  
<222> (125)..(145)  
<223> Diphtheria toxoid P30 epitope (SEQ ID NO: 14)

<220>  
<221> SIMILAR  
<222> (1)..(109)  
<223> 109 C-terminal residues of human and bovine GDF-8  
(residues 267-375 in SEQ ID NO: 1)

<220>  
<221> SIMILAR  
<222> (146)..(254)  
<223> 109 C-terminal residues of human and bovine GDF-8  
(residues 267-375 in SEQ ID NO: 1)

<220>  
<221> SITE  
<222> (90)..(91)  
<223> Lys Glu or Glu Gly

<220>  
<221> SITE

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<222> (235)..(236)

<223> Identical to (90)..(91)

<400> 22

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser Gln Tyr Ile  
100 105 110

Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Phe Asn Asn Phe  
115 120 125

Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu  
130 135 140

Glu Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys  
145 150 155 160

Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp  
165 170 175

Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys  
180 185 190

Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln  
195 200 205

Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met  
210 215 220

Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr  
225 230 235 240

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Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
245 250

<210> 23  
<211> 160  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (16)..(36)  
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
<221> MUTAGEN  
<222> (37)..(51)  
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
<221> SIMILAR  
<222> (1)..(15)  
<223> Identical to residues 216-230 of SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (52)..(160)  
<223> Identical to residues 267-375 of SEQ ID NO: 1

<220>  
<221> SITE  
<222> (124)  
<223> Cys or Ser

<220>  
<221> SITE  
<222> (141)..(142)  
<223> Lys Glu or Glu Gly

<400> 23  
Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile Lys Ala Leu Phe  
1 5 10 15

Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala  
20 25 30

Ser His Leu Glu Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile

35

40

45

Thr Glu Leu Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser  
50 55 60

Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp  
65 70 75 80

Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly  
85 90 95

Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val  
100 105 110

His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr  
115 120 125

Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile  
130 135 140

Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
145 150 155 160

&lt;210&gt; 24

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; PADRE Peptide

&lt;400&gt; 24

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala  
1 5 10